Emergence and molecular characterization of clonal complex 398 (CC398) methicillin-resistant Staphylococcus aureus (MRSA) in New Zealand

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Sir,

Of increasing public health importance is the recognition that livestock, most notably swine, poultry and veal calves, act as reservoirs of methicillin-resistant Staphylococcus aureus (MRSA) strains.1 Livestock-associated MRSA (LA-MRSA) strains can effectively colonize and infect humans, with subsequent transmission in both community and healthcare settings.2,3 To date, the most commonly reported LA-MRSA strains are those that belong to clonal complex 398 (CC398).1 Recent reports suggest that CC398 MRSA accounts for up to 25% of all community-associated MRSA in some parts of Europe.2 Moreover, CC398 MRSA has also been reported from several other geographic regions, including Singapore, China and North and Central America.2 To date, however, there have been no reports of LA-MRSA CC398 strains from New Zealand, a country noted for its strong agricultural industry. Here, we describe the first identification and molecular characterization of CC398 MRSA isolates from nine patients in New Zealand.

In New Zealand, molecular characterization of MRSA isolates is performed at the Institute of Environmental Science and Research. Molecular typing of MRSA isolates is performed by spa typing and, when necessary, isolates are further characterized by multilocus sequence typing (MLST). Between August 2011 and May 2013, MRSA isolates from nine patients were found to belong to CC398. By spa typing, these isolates were spa t011 (six isolates), spa t034 (two isolates) or spa t571 (one isolate) (Table 1). All nine patients resided in the South Island of New Zealand. Three of the patients with spa t011 CC398 either resided on a pig farm or had recently handled swine carcasses.

All isolates tested non-susceptible to penicillin, oxacillin and tetracycline. The two spa t034 isolates also tested non-susceptible to erythromycin, as did one of the spa t011 isolates (MRS13/1037), which also displayed constitutive resistance to clindamycin. The isolates were susceptible to all other tested antimicrobials. By MLST, the two spa t034 isolates were ST1232 (a single-locus variant of ST398 belonging to CC398) and all seven remaining isolates were ST398.

Further molecular characterization of MRSA isolates was performed by DNA microarray analysis (StaphType, CLONDIAG, Germany) using previously described methods.5 This demonstrated the presence of the mecA gene and the type V SCCmec element (where SCC stands for staphylococcal cassette chromosome) in all isolates. In keeping with other reports of CC398 strains, all nine isolates belonged to agr group I.6 All isolates, except the spa t571 isolate, contained the tet(K) gene, while all isolates, except the two spa t034 isolates, contained the tet(M) gene. The two spa t034 isolates contained the erm(A) gene and one of the spa t011 isolates (MRS13/1037) contained the erm(C) gene. Of note, the blaZ gene and its accompanying regulatory blal and blbR genes were not detected by DNA microarray in the two spa t034 isolates (Table 1). Tests for induced β-lactamase using nitrocefin were also negative for these two isolates, further supporting the absence of the blaZ gene.

Interestingly, both spa t034 isolates harboured the lukF-PV and lukS-PV genes encoding Panton–Valentine leukocidin (PVL). Although infrequent, human cases of PVL-positive CC398 MRSA infections have been described from Sweden, Finland and China.6,7 Of note, two of these previous cases of PVL-positive CC398 in Sweden had an epidemiological link to Asia,8 similar to one of our patients with PVL-positive spa t034 CC398 who had a recent travel history to South-East Asia.

None of the nine CC398 isolates contained genes encoding either toxic shock syndrome toxin 1 or any staphylococcal enterotoxins (Table 1). All isolates had a variety of genes encoding protein A7,7 including clfA and clfB (clumping factors A and B), cna (collagen-binding adhesin), fnbA and fnbB (fibronectin-binding proteins A and B) and bbp (bone sialoprotein-binding protein). The allelic variants of these genes were similar to those described from other CC398 strains.1,3 In addition, both PVL-positive spa t034 isolates contained genes associated with hib-converting phages, namely sak, chp and scn.

Although we did not have detailed epidemiological information on all nine patients, it is notable that three of the patients in this study had recent exposure to pigs. In other settings, isolation of CC398 MRSA has been strongly associated with exposure to livestock, including pigs, poultry and calves.2 This association with...
livestock may be of particular relevance in our geographic setting, given the large rural and agricultural sector in New Zealand.

To our knowledge, these cases represent the first known human isolations of CC398 MRSA in New Zealand. We found two clusters of CC398 MRSA, each with distinct characteristics. One cluster was due to a PVL-positive spa t034 ST1232 MRSA strain, which was associated with travel to South-East Asia, and the other cluster was due to a PVL-negative spa t011 or spa t571 ST398 strain, similar to the European LA-MRSA lineage. Ongoing clinical and molecular surveillance is essential to monitor the spread of these MRSA strains in our country.

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Transparency declarations
None to declare.

References